

REPLACEMENT SHEET



Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu  
1 5 10 15

Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His  
20 25 30

Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe  
35 40 45

Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp  
50 55 60

Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu  
65 70 75 80

Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp  
85 90 95

Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu  
100 105 110

Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala  
115 120 125

Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val  
130 135 140

Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala  
145 150 155 160

Cys Arg Thr Gly Asp  
165

*FIG. 1*

REPLACEMENT SHEET

Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu  
1 5 10 15

Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His  
20 25 30

Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe  
35 40 45

Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp  
50 55 60

Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu  
65 70 75 80

Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp  
85 90 95

Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu  
100 105 110

Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala  
115 120 125

Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val  
130 135 140

Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala  
145 150 155 160

Cys Arg Thr Gly Asp Arg  
165

**FIG. 2**

REPLACEMENT SHEET

1	GGAATTCAACCACCATGGGGTGCACGAATGTCCTGCCTGGCTGTGGCTTCCTGTCCCT CCTTAAGTGGTGGTACCCCCACGTGCTTACAGGACGGACCCGAAGAGGACAGGGA M G V H E C P A W L W L L S L -	60
61	GCTGTCGCTCCCTCTGGGCCCTCCCAGTCCTGGCGCCCCCCCCGAATCGAGGGCCGCGC CGACAGCGAGGGAGACCCGGAGGGTCAGGACCCCGGGGGGGGGCTTAGCTCCCGCGCG L S L P I G L P V L G A P P R I E G R A -	120
121	CCCACCA CGCCTCATCTGTGACAGCCGAGTCCTGGAGAGGTACCTTTGGAGGCCAAGGA GGGTGGTGC GGAGTAGACACTGTCGGCTCAGGACCTCTCCATGGAGAACCTCCGGTT CCT P P R L I C D S R V L E R Y L L E A K E -	180
181	GGCCGAGAAATATCACGACGGGCTGTGCTGAACACTGCAGCTTGAATGAGAATATCACTGT CCGGCTCTTATAGTGCTGCCCGACACGACTTGTGACGTCGAACTTACTCTTATAGTGACA A E N I T T G C A E H C S L N E N I T V -	240
241	CCCAGACACCAAAGTTAATTCTATGCCTGGAAGAGGATGGAGGTGGCAGCAGGCCGT GGGTCTGTGGTTCAATTAAAGATA CGGACCTCTCCTACCTCCAGCCCGTCGTCCGGCA P D T K V N F Y A W K R M E V G Q Q A V -	300
301	AGAAGTCTGGCAGGGCCTGGCCCTGCTGCGGAAGCTGTCTGCAGGCCAGGCCCTGTT TCTTCAGACCGTCCGGACCGGACGACAGCCTCGACAGGACGCCCGGTCCGGGACAA E V W Q G L A L L S E A V L R G Q A L L -	360
361	GGTCAACTCTTCCCAGCCGTGGAGCCCTGCAGCTGCATGTGGATAAGCCGTAGTGG CCAGTTGAGAAGGGTCGGCACCCCTGGGGACGTCGACGTACACCTATTCGGCAGTCACC V N S S Q P W E P L Q L H V D K A V S G -	420
421	CCTTCGCAGCCTCACCACTCTGCTTCGGCTCTGGAGCCAGAAGGAAGCCATCTCCCC GGAAGCGTCGGAGTGGTGAGACGAAGCCCGAGACCCCTGGGTCTTCCTCGGTAGAGGGG	480

*FIG. 3a*

REPLACEMENT SHEET

L R S L T T L L R A L G A Q K E A I S P -  
TCCAGATGCGGCCCTCAGCTGCTCCACTCCGAACAAATCACTGCTGACACTTCCGCAA  
481 -----+-----+-----+-----+-----+-----+ 540  
  
AGGTCTACGCCGGAGTCGACGAGGTGAGGCTTGTTAGTGACGACTGTGAAAGGC  
P D A A S A A P L R T I T A D T F R K L -  
  
CTTCCGAGTCTACTCCAATTCCCTCCGGGGAAAGCTGAAGCTGTACACAGGGGAGGC  
541 -----+-----+-----+-----+-----+-----+ 600  
  
GAAGGCTCAGATGAGGTTAAGGAGGCCCTTCGACTTCGACATGTGTCCCCCTCCGGAC  
F R V Y S N F L R G K L K L Y T G E A C -  
  
CAGGACAGGGACAGATGACCAGGTCGAC  
601 -----+-----+----- 629  
GTCCTGTCCCCCTGTCTACTGGTCCAGCTG  
R T G D R \* -

*FIG. 3b*

REPLACEMENT SHEET

1 GGAATTCAACCACCATGGGGTGCACGAATGTCCTGCCTGGCTGTGGCTTCCTGTCCCT  
 1-----+-----+-----+-----+-----+-----+-----+ 60  
 1 CCTTAAGTGGTGGTACCCCCACGTGCTTACAGGACGGACCGAACCGAAGAGGACAGGGA  
 1 M G V H E C P A W L W L L S L -  
 1  
 61 GCTGTCGCTCCCTCTGGGCCTCCCAGTCCTGGCGCCCCCCCCGCCACACGCCTCAT  
 61-----+-----+-----+-----+-----+-----+-----+ 120  
 61 CGACAGCGAGGGAGACCCGGAGGGTCAGGACCCGGGGGGGGGGGGGGTGGTGCAGGAGTA  
 61 L S L P L G L P V L G A P P A P P R L I -  
 121 CTGTGACAGCCGAGTCCTGGAGAGGTACCTTTGGAGGCCAAGGAGGCCGAGAATATCAC  
 121-----+-----+-----+-----+-----+-----+-----+ 180  
 121 GACACTGTCGGCTCAGGACCTCTCCATGGAGAACCTCCGGTTCTCCGGCTCTTATAGTG  
 121 C D S R V L E R Y L L E A K E A E N I T -  
 181 GACGGGCTGTGCTGAACACTGCAGCTTGAATGAGAATATCACTGTCCCAGACACCAAAGT  
 181-----+-----+-----+-----+-----+-----+-----+ 240  
 181 CTGCCCCACACGACTTGTGACGTGAACTTACTCTTATAGTGACAGGGTCTGTGGTTCA  
 181 T G C A E H C S L N E N I T V P D T K V -  
 241 TAATTTCTATGCCTGGAAGAGGATGGAGGTGGGGCAGCAGGCCGTAGAAGTCTGGCAGGG  
 241-----+-----+-----+-----+-----+-----+-----+ 300  
 241 ATTAAGATAACGGACCTTCTCCTACCTCCAGCCCCGTGTCGGCATCTCAGACCGTCCC  
 241 N F Y A W K R M E V G Q Q A V E V W Q G -  
 301 CCTGGCCCTGCTGCGAACGCTGTCCTGCGGGGCCAGGCCCTGTTGGTCAACTCTTCCCA  
 301-----+-----+-----+-----+-----+-----+-----+ 360  
 301 GGACCGGGACGACAGCCTTCGACAGGACGCCCGGTCCGGACAACCAGTTGAGAAGGGT  
 301 L A L L S E A V L R G Q A L L V N S S Q -  
 361 GCCGTGGGAGCCCTGCAGCTGCATGTGGATAAACGCCGTCACTGGCCTTCGCAGCCTCAC  
 361-----+-----+-----+-----+-----+-----+-----+ 420  
 361 CGGCACCCCTCGGGGACGTCGACGTACACCTATTCGGCAGTCACCGGAAGCGTCGGAGTG  
 361 P W E P L Q L H V D K A V S G L R S L T -  
 421 CACTCTGCTTCGGCTCTGGGAGCCAGAAGGAAGCCATCTCCCTCCAGATGCGGCCTC  
 421-----+-----+-----+-----+-----+-----+-----+ 480  
 421 GTGAGACGAAGCCGAGACCTCGGGCTTCCTCGGTAGAGGGAGGTCTACGCCGGAG  
 421 T L L R A L G A Q K E A I S P P D A A S -

**FIG. 4a**

REPLACEMENT SHEET

AGCTGCTCCACTCCGAACAATCACTGCTGACACTTCCGCAAACCTCTCCGAGTCTACTC  
481 -----+-----+-----+-----+-----+-----+ 540  
TCGACGAGGTGAGGCTTGTAGTGACGACTGTGAAAGGCCTTGAGAAGGCTCAGATGAG  
A A P L R T I T A D T F R K L F R V Y S -  
  
CAATTCCCTCCGGGAAAGCTGAAGCTGTACACAGGGAGGCCTGCAGGACAGGGACAG  
541 -----+-----+-----+-----+-----+-----+ 600  
GTTAAAGGAGGCCCTTTCGACTTCGACATGTGTCCCCTCCGGACGTCTGTCCCCGTGTC  
N F L R G K L K L Y T G E A C R T G D R -  
  
ATGACCAGGTCGAC  
601 -----+--- 614  
TACTGGTCCAGCTG  
\* -

*FIG. 4b*

REPLACEMENT SHEET

1	GGAATTCAACCACCATGGGGTGCACGAATGTCCTGCCTGGCTGTGGCTCTCCTGTCCCT CCTTAAGTGGTGGTACCCCCACGTGCTACAGGACGGACCGACACCGAAGAGGGACAGGGA M G V H E C P A W L W L L S L -	60
61	GCTGTCGCTCCCTCTGGGCCCTCCCAGTCCTGGCGCCCCCCCCGGCGCCGCCACTACGC CGACAGCGAGGGAGACCCGGAGGGTCAGGACCCGGGGGGGGCCGGCGGGTGTGCG L S L P L G L P V L G A P P G A A H Y A -	120
121	CCCACCA CGC CT CAT CT GTGACAGCCAGTCCTGGAGAGGTACCTCTGGAGGCCAAGGA GGGTGGTGC GGAGTAGACACTGTCGGCTCAGGACCTCTCCATGGAGAACCTCCGGTT CCT P P R L I C D S R V L E R Y L L E A K E -	180
181	GGCCGAGAATATCACGACGGCTGTGCTGAACACTGCAGCTTGAATGAGAATATCACTGT CCGGCTCTTATAGTGCTGCCGACACGACTTGTGACGTGAACTTACTCTTATAGTGACA A E N I T T G C A E H C S L N E N I T V -	240
241	CCCAGACACCAAAAGTTAATTCTATGCCTGGAAGAGGATGGAGGTGGGGCAGCAGGCCGT GGGTCTGTGGTTCAATTAAAGATA CGGACCTCTCCTACCTCCAGCCCGTGTCCGGCA P D T K V N F Y A W K R M E V G Q Q A V -	300
301	AGAAGTCTGGCAGGGCTGGCCCTGCTGCGGAAGCTGTCTGCAGGCCCTGTT TCTTCAGACCGTCCGGACCGGACGACAGCCTCGACAGGACGCCCGGTCCGGGACAA E V W Q G L A L L S E A V L R G Q A L L -	360
361	GGTCAACTCTCCCAGCCGTGGAGCCCTGCAGCTGCATGTGGATAAGCCGTAGTGG CCAGTTGAGAAGGGTCGGCACCCCTCGGGGACGTGACGTACACCTATT CGGCAGTCACC V N S S Q P W E P L Q L H V D K A V S G -	420
421	CCTTCGCAGCCTCACCACTCTGCTTCGGGCTCTGGGAGCCAGAAGGAAGCCATCTCCCC GGAAGCGTCGGAGTGGTGAGACGAAGCCCGAGACCCCTCGGGTCTCCTCGGTAGAGGGG L R S L T T L L R A L G A Q K E A I S P -	480

**FIG. 5a**

REPLACEMENT SHEET

481 TCCAGATGCGGCCCTCAGCTGCTCCACTCCGAACAATCACTGCTGACACTTCCGAAACT  
-----+-----+-----+-----+-----+-----+-----+-----+ 540  
AGGTCTACGCCGGAGTCGACGGAGGTGAGGCTTGTAGTGACGACTGTGAAAGGCCTTGA  
P D A A S A A P L R T I T A D T F R K L -  
  
541 CTTCCGAGTCTACTCCAATTCCCTCCGGGGAAAGCTGAAGCTGTACACAGGGGAGGCCTG  
-----+-----+-----+-----+-----+-----+-----+ 600  
GAAGGCTCAGATGAGGTTAAGGAGGCCCTTCGACTTCGACATGTGTCCCCCTCCGGAC  
F R V Y S N F L R G K L K L Y T G E A C -  
  
601 CAGGACAGGGGACAGATGACCAGGTCGAC  
-----+-----+----- 629  
GTCCTGTCCCCCTGTCTACTGGTCCAGCTG  
R T G D R \* -

**FIG. 5b**